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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/007,747

DATE: 03/20/2002

TIME: 11:52:40

Input Set : N:\Crf3\RULE60\10007747.raw

Output Set: N:\CRF3\03202002\J007747.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Daggett, Lorrie P.

3 Ellis, Steven B.

4 Liaw, Chen W.

5 Lu, Chin-Chun

6 (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

7 SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

8 (iii) NUMBER OF SEQUENCES: 63

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Heller Ehrman White & McAuliffe

11 (B) STREET: 4250 Executive Square, 7th Floor

12 (C) CITY: La Jolla

13 (D) STATE: CA

14 (E) COUNTRY: USA

15 (F) ZIP: 92037

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk

18 (B) COMPUTER: IBM PC compatible

19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/10/007,747

C--> 23 (B) FILING DATE: 07-Dec-2001

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US/09/648,797

26 (B) FILING DATE: 28-Aug-2000

27 (A) APPLICATION NUMBER: US/08/940,086A

28 (B) FILING DATE: 29-SEPT-97

29 (A) APPLICATION NUMBER: US 08/231,193

30 (B) FILING DATE: 20-APR-1994

31 (A) APPLICATION NUMBER: US 08/052,449

32 (B) FILING DATE: 20-APR-1993

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Seidman, Stephanie

35 (B) REGISTRATION NUMBER: 33,779

36 (C) REFERENCE/DOCKET NUMBER: 24735-9383C

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (619) 450-8400

39 (B) TELEFAX: (619) 450-8499

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 4298 base pairs

ENTERED

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43 (B) TYPE: nucleic acid
44 (C) STRANDEDNESS: both
45 (D) TOPOLOGY: both
46 (ii) MOLECULE TYPE: cDNA
47 (ix) FEATURE:
48 (A) NAME/KEY: CDS
49 (B) LOCATION: 262..3078
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG 60
52 CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC 120
53 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGACGCC CGCGGGGCCG GGCGAGCGCA 180
54 GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG 240
55 CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
56 Met Ser Thr Met Arg Leu Leu Thr Leu Ala
57 1 5 10
58 CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
59 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
60 15 20 25
61 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
62 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
63 30 35 40
64 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
65 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
66 45 50 55
67 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG 483
68 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
69 60 65 70
70 GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
71 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
72 75 80 85 90
73 CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
74 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
75 95 100 105
76 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
77 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
78 110 115 120
79 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675
80 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu
81 125 130 135
82 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG 723
83 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met
84 140 145 150
85 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC 771
86 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp
87 155 160 165 170
88 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG 819
89 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu
90 175 180 185
91 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG 867

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92	Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	
93	190 195 200	
94	AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
95	Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	
96	205 210 215	
97	ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA	963
98	Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	
99	220 225 230	
100	GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC	1011
101	Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly	
102	235 240 245 250	
103	GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC	1059
104	Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile	
105	255 260 265	
106	CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC	1107
107	Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser	
108	270 275 280	
109	GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG	1155
110	Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys	
111	285 290 295	
112	GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC	1203
113	Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile	
114	300 305 310	
115	TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT	1251
116	Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr	
117	315 320 325 330	
118	GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG	1299
119	Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg	
120	335 340 345	
121	AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG	1347
122	Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val	
123	350 355 360	
124	CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG	1395
125	Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys	
126	365 370 375	
127	ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG	1443
128	Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met	
129	380 385 390	
130	TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC	1491
131	Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr	
132	395 400 405 410	
133	GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC	1539
134	Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val	
135	415 420 425	
136	AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG	1587
137	Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr	
138	430 435 440	
139	TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT	1635
140	Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe	

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141				445				450				455								
142	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683			
143	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr				
144	460							465			470									
145	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731			
146	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val				
147	475							480			485				490					
148	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779			
149	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu				
150				495				500							505					
151	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827			
152	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu				
153				510				515							520					
154	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875			
155	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu				
156	525							530							535					
157	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923			
158	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe				
159	540							545							550					
160	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971			
161	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val				
162	555							560							565					
163	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019			
164	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe				
165				575				580							585					
166	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067			
167	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr				
168	590							595							600					
169	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115			
170	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly				
171	605							610							615					
172	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163			
173	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met				
174	620							625							630					
175	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211			
176	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn				
177	635							640							645					
178	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259			
179	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly				
180				655				660							665					
181	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TC										

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190	GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC	2451
191	Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile	
192	715 720 725 730	
193	TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG	2499
194	Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu	
195	735 740 745	
196	GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG	2547
197	Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met	
198	750 755 760	
199	CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG	2595
200	Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys	
201	765 770 775	
202	TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG	2643
203	Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg	
204	780 785 790	
205	TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT	2691
206	Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe	
207	795 800 805 810	
208	GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC	2739
209	Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala	
210	815 820 825	
211	GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT	2787
212	Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp	
213	830 835 840	
214	GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG	2835
215	Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp	
216	845 850 855	
217	CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT	2883
218	Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro	
219	860 865 870	
220	AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC	2931
221	Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser	
222	875 880 885 890	
223	TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC	2979
224	Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg	
225	895 900 905	
226	GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT	3027
227	Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile	
228	910 915 920	
229	GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC	3075
230	Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser	
231	925 930 935	
232	TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCGCA GACAGACAGA CAGACGGACG	3135
233	GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
234	CCAGCCTCCC CCAGGCTGCG CCTGCCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
235	GTCCCGGCC CGCGGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGCTCT GTGTATTCTCT	3315
236	ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCG TCAACCTCTC AGATCCCTCG	3375
237	GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
238	ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18
Seq#:47; N Pos. 18
Seq#:49; N Pos. 18
Seq#:51; N Pos. 18
Seq#:53; N Pos. 18
Seq#:57; Xaa Pos.1147,1171
Seq#:58; Xaa Pos.1147,1171

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1493 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1499 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1508 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1517 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1529 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1535 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2813 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2816 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2819 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2822 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2825 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2828 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2834 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2837 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2840 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
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L:2852 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2864 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25

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Input Set : N:\Crf3\RULE60\10007747.raw

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L:3058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:9138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:3937
L:9144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:4033
L:9330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1136
L:9334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1168